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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2011; month=1; day=21; hr=9; min=7; sec=0; ms=643; ]

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Application No: 10528183 Version No: 2.0

**Input Set:****Output Set:**

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**Finished:** 2011-01-11 14:43:04.929  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 138 ms  
**Total Warnings:** 106  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 106  
**Actual SeqID Count:** 106

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**Input Set:**

**Output Set:**

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**No. of SeqIDs Defined:** 106  
**Actual SeqID Count:** 106

Error code

Error Description

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# SEQUENCE LISTING

<110> Ullman, Katharine  
Liu, Jin  
Prunuske, Amy  
Dimaano, Christian

<120> METHODS OF INHIBITING CELL CYCLE OF A CELL COMPRISING ADMINISTERING  
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<130> 21101.0045U2

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<141> 2005-05-27

<150> PCT/US2003/29267

<151> 2003-09-17

<150> 60/411248

<151> 2002-09-17

<160> 106

<170> PatentIn version 3.5

<210> 1

<211> 5687

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Note = Synthetic Construct

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35 40 45

Asn Ile Val Pro Gly Trp Leu Gln Arg Tyr Phe Asn Lys Asn Glu Asp  
50 55 60

Val Cys Ser Cys Ser Thr Asp Thr Ser Glu Val Pro Arg Trp Pro Glu  
65 70 75 80

Asn Lys Glu Asp His Leu Val Tyr Ala Asp Glu Glu Ser Ser Asn Ile  
85 90 95

Thr Asp Gly Arg Ile Thr Pro Glu Pro Ala Val Ser Asn Thr Glu Glu  
100 105 110

Pro Ser Thr Thr Ser Thr Ala Ser Asn Tyr Pro Asp Val Leu Thr Arg  
115 120 125

Pro Ser Leu His Arg Ser His Leu Asn Phe Ser Met Leu Glu Ser Pro  
130 135 140

Ala Leu His Cys Gln Pro Ser Thr Ser Ser Ala Phe Pro Ile Gly Ser  
145 150 155 160

Ser Gly Phe Ser Leu Val Lys Glu Ile Lys Asp Ser Thr Ser Gln His  
165 170 175

Asp Asp Asp Asn Ile Ser Thr Thr Ser Gly Phe Ser Ser Arg Ala Ser  
180 185 190

Asp Lys Asp Ile Thr Val Ser Lys Asn Thr Ser Leu Pro Pro Leu Trp



195

200

205

Ser Pro Glu Ala Glu Arg Ser His Ser Leu Ser Gln His Thr Ala Thr  
210 215 220

Ser Ser Lys Lys Pro Ala Phe Asn Leu Ser Ala Phe Gly Thr Leu Ser  
225 230 235 240

Pro Ser Leu Gly Asn Ser Ser Ile Leu Lys Thr Ser Gln Leu Gly Asp  
245 250 255

Ser Pro Phe Tyr Pro Gly Lys Thr Thr Tyr Gly Gly Ala Ala Ala Ala  
260 265 270

Val Arg Gln Ser Lys Leu Arg Asn Thr Pro Tyr Gln Ala Pro Val Arg  
275 280 285

Arg Gln Met Lys Ala Lys Gln Leu Ser Ala Gln Ser Tyr Gly Val Thr  
290 295 300

Ser Ser Thr Ala Arg Arg Ile Leu Gln Ser Leu Glu Lys Met Ser Ser  
305 310 315 320

Pro Leu Ala Asp Ala Lys Arg Ile Pro Ser Ile Val Ser Ser Pro Leu  
325 330 335

Asn Ser Pro Leu Asp Arg Ser Gly Ile Asp Ile Thr Asp Phe Gln Ala  
340 345 350

Lys Arg Glu Lys Val Asp Ser Gln Tyr Pro Pro Val Gln Arg Leu Met  
355 360 365

Thr Pro Lys Pro Val Ser Ile Ala Thr Asn Arg Ser Val Tyr Phe Lys  
370 375 380

Pro Ser Leu Thr Pro Ser Gly Glu Phe Arg Lys Thr Asn Gln Arg Ile  
385 390 395 400

Asp Asn Lys Cys Ser Thr Gly Tyr Glu Lys Asn Met Thr Pro Gly Gln  
405 410 415

Asn Arg Glu Gln Arg Glu Ser Gly Phe Ser Tyr Pro Asn Phe Ser Leu  
420 425 430

Pro Ala Ala Asn Gly Leu Ser Ser Gly Val Gly Gly Gly Gly Gly Lys  
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Met Arg Arg Glu Arg Thr Arg Phe Val Ala Ser Lys Pro Leu Glu Glu  
450 455 460

Glu Glu Met Glu Val Pro Val Leu Pro Lys Ile Ser Leu Pro Ile Thr  
465 470 475 480

Ser Ser Ser Leu Pro Thr Phe Asn Phe Ser Ser Pro Glu Ile Thr Thr  
485 490 495

Ser Ser Pro Ser Pro Ile Asn Ser Ser Gln Ala Leu Thr Asn Lys Val  
500 505 510

Gln Met Thr Ser Pro Ser Ser Thr Gly Ser Pro Met Phe Lys Phe Ser  
515 520 525

Ser Pro Ile Val Lys Ser Thr Glu Ala Asn Val Leu Pro Pro Ser Ser  
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Ile Gly Phe Thr Phe Ser Val Pro Val Ala Lys Thr Ala Glu Leu Ser  
545 550 555 560

Gly Ser Ser Ser Thr Leu Glu Pro Ile Ile Ser Ser Ser Ala His His  
565 570 575

Val Thr Thr Val Asn Ser Thr Asn Cys Lys Lys Thr Pro Pro Glu Asp  
580 585 590

Cys Glu Gly Pro Phe Arg Pro Ala Glu Ile Leu Lys Glu Gly Ser Val  
595 600 605

Leu Asp Ile Leu Lys Ser Pro Gly Phe Ala Ser Pro Lys Ile Asp Ser  
610 615 620

Val Ala Ala Gln Pro Thr Ala Thr Ser Pro Val Val Tyr Thr Arg Pro  
625 630 635 640

Ala Ile Ser Ser Phe Ser Ser Ser Gly Ile Gly Phe Gly Glu Ser Leu  
645 650 655

Lys Ala Gly Ser Ser Trp Gln Cys Asp Thr Cys Leu Leu Gln Asn Lys  
 660 665 670

Val Thr Asp Asn Lys Cys Ile Ala Cys Gln Ala Ala Lys Leu Ser Pro  
 675 680 685

Arg Asp Thr Ala Lys Gln Thr Gly Ile Glu Thr Pro Asn Lys Ser Gly  
 690 695 700

Lys Thr Thr Leu Ser Ala Ser Gly Thr Gly Phe Gly Asp Lys Phe Lys  
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Pro Val Ile Gly Thr Trp Asp Cys Asp Thr Cys Leu Val Gln Asn Lys  
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Pro Glu Ala Ile Lys Cys Val Ala Cys Glu Thr Pro Lys Pro Gly Thr  
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Cys Val Lys Arg Ala Leu Thr Leu Thr Val Val Ser Glu Ser Ala Glu  
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Thr Met Thr Ala Ser Ser Ser Ser Cys Thr Val Thr Thr Gly Thr Leu  
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Gly Phe Gly Asp Lys Phe Lys Arg Pro Ile Gly Ser Trp Glu Cys Ser  
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 820 825 830

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Lys Ala Asp Ser Thr Lys Cys Leu Ala Cys Glu Ser Ala Lys Pro Gly  
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Thr Lys Ser Gly Phe Lys Gly Phe Asp Thr Ser Ser Ser Ser Ser Asn  
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Ser Ala Ala Ser Ser Ser Phe Lys Phe Gly Val Ser Ser Ser Ser Ser  
900 905 910

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915 920 925

Gln Gly Gly Phe Lys Ile Gly Val Ser Ser Asp Ser Gly Ser Ile Asn  
930 935 940

Pro Met Ser Glu Gly Phe Lys Phe Ser Lys Pro Ile Gly Asp Phe Lys  
945 950 955 960

Phe Gly Val Ser Ser Glu Ser Lys Pro Glu Glu Val Lys Lys Asp Ser  
965 970 975

Lys Asn Asp Asn Phe Lys Phe Gly Leu Ser Ser Gly Leu Ser Asn Pro  
980 985 990

Val Ser Leu Thr Pro Phe Gln Phe Gly Val Ser Asn Leu Gly Gln Glu  
995 1000 1005

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1025 1030 1035

Ile Val Thr Ser Glu Asn Lys Ser Ser Phe Asn Leu Gly Thr Ile  
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1070 1075 1080

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Val Leu Gly Arg Thr Glu Glu Lys Gln Gln Glu Pro Val Thr Ser

1100

1105

1110

Thr Ser Leu Val Phe Gly Lys Lys Ala Asp Asn Glu Glu Pro Lys  
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Cys Gln Pro Val Phe Ser Phe Gly Asn Se